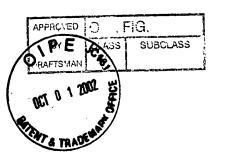
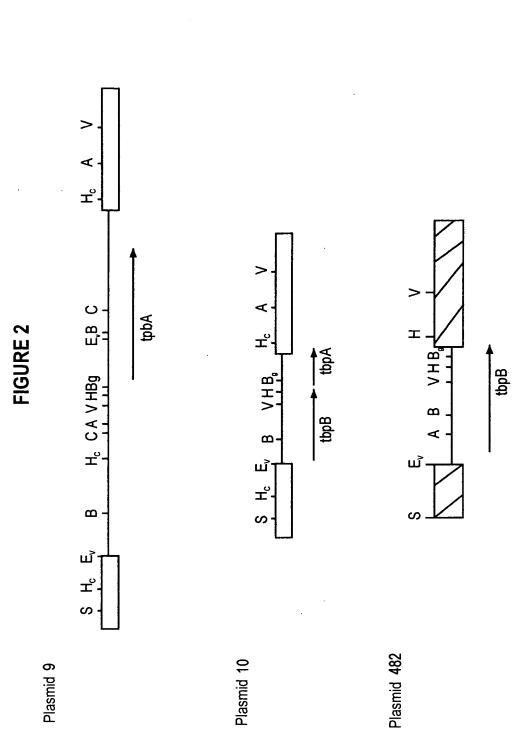




FIGURE 1A

FIGURE 1B





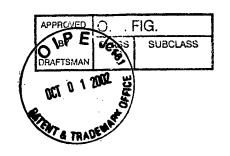


FIGURE 3A

tbpB

	10	20	30	40	50
1	CGCTTGCAGA	TTTGTAAAAA	ATTTAGCTAA	AATCAGACCT	GGCTTGTATT
51	TTAGGGTTAT	TATGGAACAG	ACAACGGAAC	AAATAGATTA	TAAATTATTA
101	AAGCATCGTT	TTCGTGGCTA	TTTACCGCTT	GTGATTGATG	TGGAACAGAG
151	GCTTAAATGC	CCAAACTGTG	CCTTATTGGA	ATTGGCCGGA	ATTACTTTAA
201	AATTGGACGA	GCCAAGGTTA	TCTTATTGCC	GGATTCAACA	ATGCCAATTT
251	CCAATTTGCG	GCCATTGGAG	GGGGCGATTT	TCAAGGGCCG	AATATTTACC
301	CTCAGTCATT	AAAATTCAAC	GGCATTCATA	TTCACAACCC	TCTAGAGGAA
351	GCGGTTTAGA	GAATATTGCC	CAATTCCCGG	AAATGTTCAA	AATGGTTCGC
401	AAAGCAATGA	AGGAAGCAAG	GCTGCCAACG	GGCGGTGATT	GTTGCCCCAC
451	AATGCCAGCG	TTCGATCAGG	GCTTTTTTAC	AGGGCTGCGA	TTAAACGGAA
501	TGCCAAGCGA	GAGATCCCTT	TCACCCTTTT	GGCGATGTTT	GACTACCGCC
551	GCCACCCTTT	GCAGGTTTTA	TGTTATGGGC	AAACCGTGTT	CGTTAAAAGC
601	CTGCCAGTGC	AAAATCCGTT	CACGTAGCAG	CACTATAGGG	CGAATTGGGT
651	ACCGGGCCCC	CCTCGAGGTC	GACGGTATCG	ATAAAGCTTC	ATATCGAATT
701	CCTGCAGCCC	GGGGGATCCG	ATGCGCCTTG	CGGCTCAAGT	TATTAGTGGC
751	ATCGGTTTTT	TGGGTGATGG	TGTCATTTTG	CATAAGAAAA	ATGATGCGAT
801	TTCAGGTTTA	CCCACTGCGG	CGATTATTTG	GGCTTCTGCG	GGGATCGGTA
851	TTGCTGCAGG	GGAGGGTTTC	GTGTTTCATG	CGGTCATCGC	CACTGTCATT
901	ATTTTGGTGT	CTATTCGATT	ATGTCCGTTG	GTTCAACGTT	GGGTTCATCG
951	TAAATCACAA	CGTCGTCGAC	GAAATATTCT	TGTCAATGAT	GCGGAAAGCA
1001	TACGGAAAGT	TACCCAATIG	TTATTCAATA	ATCAGTATCG	TATTGAACAT
1051	ATACAAGTCA	AAGATCAAAG	TAGTGGAGAA	GTTGCCGGTT	ACAAATTCGT

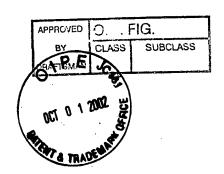


FIGURE 3B

1101 ATTGATTCCA CAATGTTCAA AGATGCGTAT GCTTTACTTA AAGCAGAAGA 1151 TGGCGAATAC TGTTCAAGTA GATATCATGA AAAAGAGTGC TTATATTCAA 1201 TTTTTTATTT TTTATTTAAT TTCTTTCCAC AAAAGATCAT TTTCAATTAT 1251 ATATACTGGA ATTTTGCCTT ACGCTATCTG TCATTTATTA TGCTATTCAA 1301 GCACAACAAA CTATGGAACA ACAATCAAAA TGTACGCTTA TCGGCTGCCG 1351 ATGATTTCGA TAATGATCGA TGTGCAGAAA TATTTGAACT TACGATTTTC 1401 ACTGAGCAGT CAAAGCACGT TCGCGAGTAT CGACTCTACT TTATTTATCG 1451 TTTGTGCACT ATGTATAATC CACCTAATTC CGTGCCTTGG CCATAAAAGC 1501 CCCCTTCAAA FTGTATTTAT ATCAGCTACC GTGCCACCAT TCGTACTTTT 1551 CGGATCAAGA TTAAAACAGA ATCCCTGCAT GCACAGCGAA ATCAGCTGCG 1601 GTATGCGAAA CGCCGCAGGA GCGCAGTACG CGAAGTGTAC CGTCACTATC 1651 AGTGCTAGAT TTGTCAATAA AAAATTAGTG ACCAAGCTTG GGTGCATAAT 1701 GATGGTGATG AAAGAACGCT CAATGCTTGA CACGTTGCAG GCTATCTGTA 1751 AGGGTATGGT AGTTACAGGC ACAGCCCAAA CGGCCAATTG CTGGTTTTTT 1801 ATCCTTGATC CGAACAGTAC GAATGGTGGT CACGGTAGTG CATATACATA 1851 CTCAATTGAA GGGGGCTTTT ATGGCCCTAA GGCGACGGAA TTAGGTGGTA 1901 TTGTACATAG TGCAGAAACG GATAAAGATA GAGTCAGTAT TACATTCGGC 1951 GGAAAACGTC AAATAGAAAA ATAATCATAA TTCCCCTTTG CTGGTTGTAG 2001 ATAGCAGCGG GCAATTTTTT ATAAAAATTT GCAAAATTTA AATAA

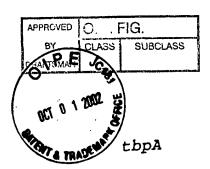


FIGURE 3C

	10	20	30 1	40	50
. 1	AGACCCTATC	TAATGATAAT	GAAATATCAT	CATTTTCGCT	ATTCACCTGT
51	TGCCTTAACA	GTGTTATTTG	CTCTTTCTCA	TTCATACGGT	GCTGCGACTG
101	AAAATAAAA	AATCGAAGAA	AATAACGATC	TAGCTGTTCT	GGATGAAGTT
151	ATTGTGACAG	AGAGCCATTA	TGCTCACGAA	CGTCAAAACG	AAGTAACTGG
201	CTTGGGGAAA	GTAGTGAAAA	ATTATCACGA	AATGAGTAAA	AATCAAATTC
251	TTGGTATTCG	TGATTTAACT	CGCTATGACC	CTGGTATTTC	GGTGGTGGAA
301	CAAGGTCGCG	GTGCAAGTAG	TGGCTATGCC	ATTCGAGGTG	TAGATAAAAA
351	CCGTGTCAGC	TTACTTGTTG	ATGGGCTACC	ACCAGCGCAC	AGTTATCATA
401	CGCTGGTTCA	GATGCTAATG	GTGGTGCAAT	TAATGAGATT	GAGTATGAAA
451	ACATTCGTTC	AATTGAGTTA	AGCAAAGGAG	CAAGTTCTGC	GGAATATGGC
501	TCTGGTGCGC	ATGGTGGTGC	TATTGGTTTT	CGTACTAAAG	ATCGCCAGGA
551	TATTATTAAA	GAGGGGCAGC	ATTGGGGCTT	ACATAGTAAG	ACCTCTTATG
601	CCAGCAAAAA	TAGCCATTTT	TACAGTCTAT	CGCAGCGGCT	GGTCAGGCGG
. 651	GTGGTTTTCA	AGCACTIGTT	ATTGCAACTC	ACCGACACGG	TAAAGAGACC
701	AAAATTCATT	CCGAGGCAAA	TCAATTACAT	ATTATTCGGC	GTATAACCGG
751	CTTTCAAAAT	CGCTACGACT	TTACCCAATT	CCGCACAGAA	TGCCTCCTGG
801	AGGATCTTTT	TTTATTGTGG	AAGATACTTG	CCCAACATTA	GATTGTACTC
851	CTCGTGCAAG	GGTTAAGTTG	AACGCGATAA	TTTCCCAGTC	AGAACATTTC
901	CGAATATACG	CCTGGAAGAG	GCGAAACAGC	TTGAGATTCC	TTATCGCACT
951	GAGCTCTCAG	CCCAAAGAAT	ARACCGGTAA	AGATCGCATT	GCACCAAACC
1001	CTTTAGATTA	CAAGAGTAAT	TCTGTTTTTA	TGAAGTTTGG	CTATCACTTT
1051	ACCTCGTCTC	ATTATCTTGG	CGCATCTCAC	AAGATGATAC	AAAACAACGC
1101	ACGATATCCG	TCATSTGCAA	ACGCCAGCTT	ACTATACAAA	AGACGATATT
1151	TACTTATCAC	TTTGGAACTA	TGTTTATCAA	GGGGATATTA	TTTAGATGGC
1201	TTAGTGTTCA	AGCCAAGGAT	CCCTTATGGG	TTGCGCATAT	GCCATGTGAA

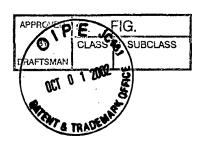


FIGURE 3D

1251	CGTCACCACA	AACGTCGTTT	AGGATTCACC	TATAAATATA	AACCAGAGAA
1301	TAATCGCTGG	TTGGATAGCA	TTAACTCGTG	CGTACGTGCT	TTGCGCTCTC
1351	GCTGCTGTGC	TCTGAGTAAA	CAAGATATTG	AACTATATAG	CCGGCTACAT
1401	CGCTTGCATT	GTAGCGATTA	TCCTGTGGTA	GATAAAAATT	GCGGCCCGAC
1451	TTTGGATAAA	TCTGGTCTAT	GTATCGAACT	GAGCGTAATA	ATTACCAAGA
1501	AAAGCATCGT	GTCATTCATT	TAGAATTTGA	TAAAGCGCTA	AATGCTGGTC
1551	AAGGCGTATT	TAAGCAAACC	CACAAACTGA	ATTTAGGCTT	GGGCTTTGAA
1601	TCGATTAATC	GCTTATGATC	ATGGGGATAT	GACTGCCCAA	TATACCAAAG
1.651	GCCGGTTATA	CCAGCTACCG	CGGAGAGGGG	CTTTAGATAA	TCCATATATT
1701	TATCGCCGCG	ATCCACGCAG	TATTGAAACG	GTATCTTTGT	GTAATAATAC
1751	AGCGGCGACA	CTTAACTGTG	ACGCGTTAAA	TAAAGGCATA	CGTTTGTACC
1801	TCCGCTGCAC	TTAGGAACTA	TAGTTTATGA	AGGGGATAAT	ATTTAGATGG
1851	CTTAGTGTTC	AAGCAAGCAA	GGATCCCTTA	TGGGTTGCGC	GATATGCCAT
1901	GTGAAGTTTT	TGATGAACGT	CACCACAAAC	GTCGTTTAGG	ATTCACACCT
1951	ATAAATATAT	AAACCAGAGA	ATAATCGCTG	GTTGGATAGC	ATTAACTCGT
2001	GCGTACGTGC	TTTGCGCTCT	CGCTGCTGTG	CTGTGAGTTA	AACAAGATAT
2051	TGAAACTTAT	AGCCGGCTAC	ATCGCTTGCA	TTGTGAGCGA	TTATCCTGTG
2101	GTAGTAGTAA	AAATTGCGGC	CCGACTTTGG	ATAAATCTTG	GTCTATGTAT
2151	CGAACTGAGC	GTAATAATTA	CCAAGAAAAG	CATCGTGTCA	TTCATTTAGA
2201	ATTTGATAAA	GCGCTAAATG	CTGGTCAAGG	CGTATTTAAG	CAAACCCACA
2251	AACTGAATTT	AGGATTGGGC	TTTGAATCGA	TTAATTCGCT	TATGGATCAT
2301	GGGGATATGA	CTGCCCAATA	TACCAAAGGC	CGGTTATACC	AGCTAACCGC
2351	GAGAGGGCGT	TTAGATAATC	CATATTTATC	GCCGCGATCC	ACGCAGTATT
2401	GAAACGGTAT	CTTTGTGTAA	TAATACACGC	GCGACACTAA	CTGTGACGCG
2451	TTAAATAAAG	GCATACGTTT	GTACCTCCGC	TGCTGCCTAA	TAAATCAAAA
2501	GAATAACCGA	GATACGGTTC	AGTGTTGTTC	CAACCAGTTG	CGATGGCCCA

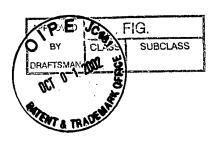


FIGURE 3E

2551 CTACGTGAAC CATCACCCTA ATCAAGTTTT TTGGGGTCGA GGTGCCGTAA
2601 AGCACTTAAC CCTTCTGTCG TCTCCCGTGG ATGCTTAAAT TCGCAGCTAG

2651 TGGCAGGCAG GCACGTCACT CCTCTCGGTG ATTTCAGGTG CAACTGACCG
2701 GTTCTTGGTA CCACCCTTGA TATTAACCGG AGTCAATTAT AAAAACGAGT

2751 TACGTGGAGC GCAATTTATA ATGTCGATGT CAGATACTGT AAAACTCTAT

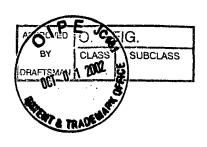
2801 ATTACCGTGG GCAGCAATTA GGTGACAGGG CCACGGGGCA AGCGAAACCA

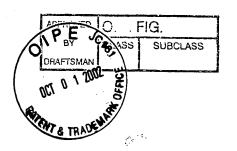
2851 GACGGGTACC AATTACACCG ATTTGCCGCC CCCGGGAGAG AAATTTCAGT

2901 TACCATTCAA AGAAGTTTAG AGCCGGCCAA AAGAAAATAC AAAAAACGCT

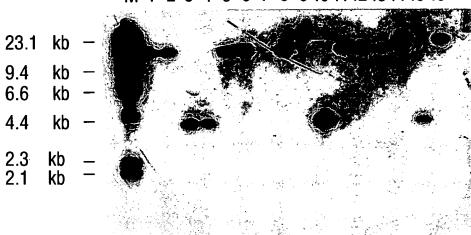
2951 GAAAGTATAT TCAGCGCGGTT TTTGTTGCTC TAACGGATTA CATACGAATT

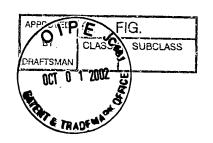
3001 CAAAATGTTT TAACGGTCGG TTA



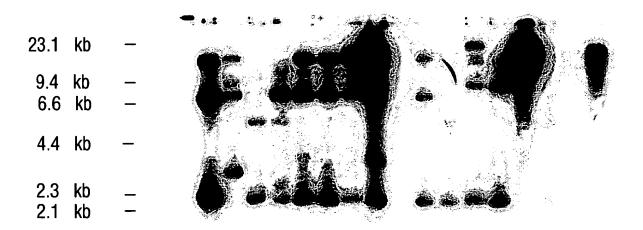


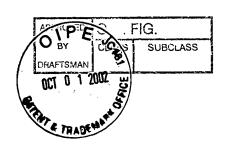
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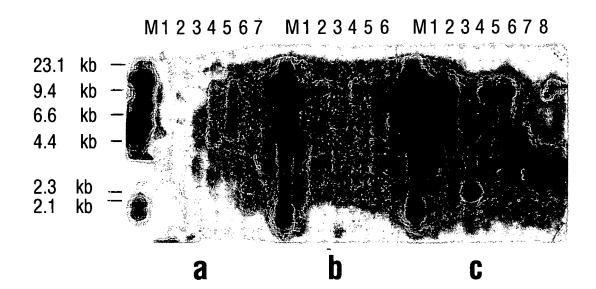




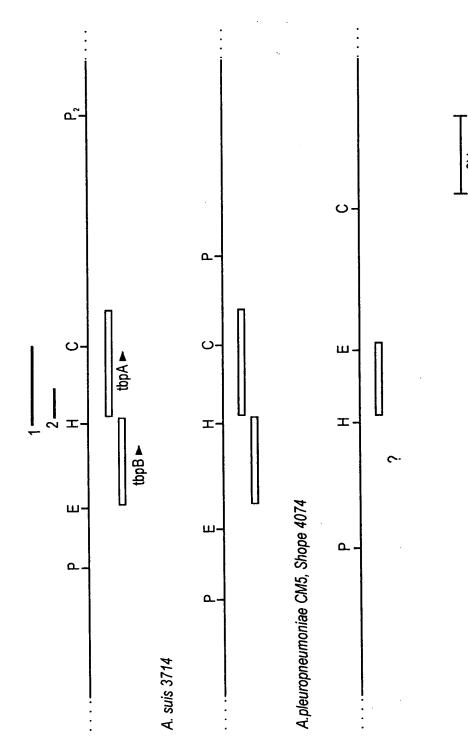
1 2 3 4 5 6 7 8 9 10 11 13 14 15 16 12







P. haemolyitca A1



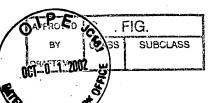


FIGURE 9A

TBP	MIMKYHHFRYSTVALTVLFALSHSYGAATENKKIEENNDLAVLDEVIVTE	50
NGTBP1	MOQO-HLFRLNILCLSLMTALP-AYAENVOAGOAOEKOLDTIQVKA	44
NM1	MQQQ-HLFRLNILCLSLMTALP-VYAENVQAEQAQEKQLDTIQVKA	44
	* . * ** * *	
PHTBP	SHYAHERQNEVTGLGKVVKNYHEMSKNQILGIRDLTRYDPGISVVEQGRG	100
NGTBP1	KKQKTRRDNEVTGLGKLVKTADTLSKEQVLDIRDLTRYDPGIAVVEQGRG	94
NM1	KKQKTRRDNEVTGLGKLVKSSDTLSKEQVLNIRDLTRYDPGIAVVEQGRG *.********.****.*.************	94
PHTBP	ASSGYAIRGVDKNRVSLLVDGLPQAHSYHTLSGDANGGAINEIE	144
NGTBP1	ASSGYSIRGMDKNRVSLTVDGLAQIQSYTAQAALGGTRTAGSSGAINEIE	144
NM1	ASSGYSIRGMDKNRVSLTVDGVSQIQSYTAQAALGGTRTAGSSGAINEIE	144
	*****.******* ***.* . *.*******	
PHTBP	YENIRSIELSKGASSAEYGSGAHGGAIGFRTKDAQDIIKEGQHWGLDSKT	194
NGTBP1	YENVKAVEISKGSNSVEQGSGALAGSVAFQTKTADDVIGEGRQWGIQSKT	194
NM1	YENVKAVEISKGSNSSEYGNGALAGSVAFQTKTAADIIGEGKQWGIQSKT ****.*** * * .** .**.*.*.* * *****	194
PHTBP	SYASKNSHFLQ-ÏAAAGEAGGFEALVIATHRHGKETKIHSEANKLKHNIR	243
NGTBP1	AYSGKNRGLTQSIALAGRIGGAEALLIRTGRHAGEIRAHEAAGRGVQSFN	244
NM1	AYSGKDHALTQSLALAGRSGGAEALLIYTKRRGREIHAHKDAGKGVQSFN .** * .* ** ** ***.* * * * *	244
PHTBP	RITGFENRYDFTQIPHRMPPGGSFFIVEDTCPTLDCTPRARVKLNRD	290
NGTBP1	RLAPVDDGSKYAYFIVEEECKNGGHE-KCKANPKKD	279
NM1	RLVLDEDKKEGGSQYRYFIVEEECHNG-YA-ACKNKLKED * * .*****	282
PHTBP	NFPVRTFPEYTPEERNAEQIPYRTEQLSAQEKTGKDRIAPNPLDYKSNSV	340
NGTBP1	VVGEDKRQTVSTRDYTGPNRFLADPLSYESRSW	312
NM1	ASVKDERKTVSTQDYTGSNRLLANPLEYGSQSW	315
PHTBP	FMKFGYHFNSS-HYLGAILEDTKQR-TISVICKRQLTIQKTILTYHLGTM	388
NGTBP1	${ t LFRPGFRFENKRHYIGGILERTQQTFDTRDMTVPAFLTKAVFDANQKQAG}$	362
NM1	LFRPGWHLDN-RHYVGAVLERTQQTFDTRDMTVPAYFTSEDYVPG * **.*. *.*	359
PHTBP	FMKGIIFRWLSVQAK-DPLWVAHMPCEVDERHHKRRLGF	426
NGTBP1	SLRGNGNHKYAGNHKYGGLFTSGENNAPVGAEYGTGVFYDETHTKSRYGL	412
NM1	SLKGLGKYSGDNKAERLFVQGEGSTLQGIGYGTGVFYDERHTKNRYGV * * * * * * *	407

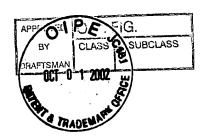


FIGURE 9B

PHTBP NGTBP1 NM1	TYKY-KPENNRWLDSINSCVRALRSRCCALSKQDIELYSRLHRLHCSDYP EYVYTNADKDTWADYARLSYDRQGIGLDNHFQQTHCSA-D EYVYHNADKDTWADYARLSYDRQGIDLDNRLQQTHCSH-D .* * * * * * * .*. * * **	475 451 446
PHTBP NGTBP1 NM1	VVDKNCGPTLDKSWSMYRTERNNYQEKHRVIHLEFDLALNAGQGVFLQTH GSDKYCRPSADKPFSYYKSDRVIYGESHKLLQAAFKKSFDTAKIRH GSDKNCRPDGNKPYSFYKSDRMIYEESRNLFQAVFKKAFDTAKIRH ** * * * * *	525 497 492
PHTBP NGTBP1 NM1	KLNLGLGFESINSLMDHGDMTAQYTLGRLYQLPRRDPRSIWTVSLCN NLSVNLGYDRFGSNLRHQDYYYQSAN-RAYSLKTPPQNNGKKTSPNGREK NLSINLGYDRFKSQLSHSDYYLQNAV-QAYDLITPKKPPFPNGSKD .*** * . * * * *	572 546 537
PHTBP NGTBP1 NM1	NTRATLNCDAL-NLGIRLYLRCCLINQLNNPRYGSVLFQFGTRV NPYWVSIGRGNVVTRQICLFGNNTYTDCTPRSINGKSYYAAVRDNVRL NPYRVSIGKTTVNTSPICRFGNNTYTDCTPRNIGGNGYYAAVQDNVRL * * . * . * * . * * * * * * * * *	615 594 585
PHTBP NGTBP1 NM1	HRTWTPTSLGELPSIRAMAHYVNHHPNQVFWGRGAVKHLTLLSS GR-WADVGAGLRYDYRSTHSDDGSVSTGTHRTLSWNAGIVLKPA GR-WADVGAGIRYDYRSTHSEDKSVSTGTHRNLSWNAGVVLKPF * * * . * . * . * . * . * . * . *	659 637 628
PHTBP NGTBP1 NM1	PWM-LKFAASGRHVTLSVISG-ATDRFLVPPLILTGVNYKNESYV DWLDLTYRTSTGFRLPSFAEMYGWRSGDKIKAVKIDPEKSFNKEAGIVFK TWMDLTYRASTGFRLPSFAEMYGWRAGESLKTLDLKPEKSFNREAGIVFK * * *	702 687 678
PHTBP NGTBP1 NM1	SAIYNVDVRYCKTLYYRGQQLGDRATGQAKPDGYQLHRFA GDFGNLEASWFNNAYRDLIVRGYEAQIKDGKEQVKGNP-AYLNAQSARIT GDFGNLEASYFNNAYRDLIAFGYETRTQNGQTSASGDP-GYRNAQNARIA * * * * *	742 736 727
PHTBP NGTBP1 NM1	APGRNFSYHSKKFRPAKENTKNAESIFS GINILGKIDWNGVWDKLPEGWYSTFAYNRVRVRDIKKRADRTDIQSHLFD GINILGKIDWHGVWGGLPDGLYSTLAYNRIKVKDADIRADRTFVTSYLFD	770 786 777
PHTBP NGTBP1 NM1	AFFVGSNGLHTNSKSCFNGRLHEPIPYFFNFLRNVPRFNEYHCCC AIQPSRYVVGSGYDQPEGKWGVNGMLTYSKAKEITELLGSR AVQPSRYVLGLGYDHPDGIWGINTMFTYSKAKSVDELLGSQ * * *	815 827 818

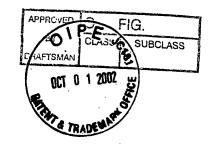


FIGURE 9C

PHTBP NGTBP1 NM1	TSLIAASILLHHIYHWVFDFRYYYFVYFCWILHHLIHINSFLMLLSHY -ALLNGNSRNTKATARRTRPWYIVDVSGYYTVKKHFTLRAGVYNLLNHRY -ALLNGNANAKKAASRRTRPWYVTDVSGYYNIKKHLTLRAGVYNLLNYRY	863 876 867
	.** * *. * * .*	
PHTBP	REVVYLTCCACAFNIVTVNGFCVGCCSNILAEMKF 898	
NGTBP1	VTWENVRQTAAGAVNQHKNVGVYNRYAAPGRNYTFSLEMKF 917	
NM1	VTWENVRQTAGGAVNQHKNVGVYNRYAAPGRNYTFSLEMKF 908	
	* * * * * * ***	

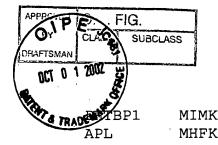


FIGURE 10A

APL APL7	MIMKYHHFRYSTVALTVLFALSHSYGAATENKKIEENNDLAVLDEVIVTE MHFKLNPYALAFTSLFLVACSGGKGSFDLEDVRPNQ MHFKLNPYALAFTSLFLVACSGGKGSFDLEDVRPNK * .** .*	50 36 36
PHTBP1 · APL APL7	SHYAHERQNEVTGLGKVVKNYHEMSKNQILGIRDLTRYDPGISVVE TAKAEKATTSYQDEETKKKTKEELDKLMEPALGYETQILRRNKAPKTETG TTGVSKEEYKDVETAKKEKEQLGELMEPALGYVVKVPVSSFE	96 86 78
PHTBP1 APL APL7	QGRGASSGYAIRGVDKNRVSLLVDGLPQAHSYHTLSGDANGGAINEI-EY EKRNERVVELSEDKITKLYQESVEIIPHLDELNGKTTSNDVYHS NKKVDISDIEVITNGNLDDVPYKANSSK-YNY	145 130 109
PHTBP1 APL APL7	ENIRSIELSKGASSAEYGSGAHGGAIGFRTKDAQ-DIIKEG HDSKRLDKNRDLKYVRSGYVYDGSFNEIRRNDSGFHVFKQGIDGYVYYLG PDIKTKDSSLQYVRSGYVIDGEHSGSNEKGYVYYKG	185 180 145
PHTBP1 APL APL7	QHWGLDSKTSYASKNSHFLQIAAAGEAGGFEALVIATHRH VTPSKELPKGKVISYKGTWDFVSNINLEREIDGFDTSGDGKNVSATSITE NSPAKELPVNQLLTYTGSWDFTSNANLNNEEGRPNYLNDDYYTK**	225 230 189
PHTBP1 APL APL7	GKETKI-HSEANKLKHNIRRITGFENRYDFTQIPHRMPPGGSFFIVED TVNRDHKVGEKLGDNEVKGVAHSSEFAVDFDNKKLTGSLYRNGYINRN FIGKRVGLVSGDAKPAKHKYTSQFEVDFATKKMTGKLSD	272 278 228
PHTBP1 APL APL7	TCPTLDCTPRARVKLNRDNFPVRTFPEYTPEERNAEQIPYRTEQLSAQ KAQEVTKRYSIEADIAGNRFRGKAKAEKAGDPIFT-DSNYLEGG KEKTIYTVNADIRGNRFTGAATASDKNKGKGESYNFFSADSQSLEGG	320 321 275
PHTBP1 APL APL7	EKTGKDRIAPNPLDYKSNSVFMKFGYHFNSSHYLGAILEDTKQRTISVIC FYGPKAEEMAGKFFTNNKSLFAVFAAKSENGETTTERIIDATKIDLTQFN FYGPKAEEMAGKFVANDKSLFAVFSAKHNGSNVNTVRIIDASKIDLTNFS . * *	370 371 325
PHTBP1 APL APL7	KRQLTIQKTILTYHLGTMFMKGIIFRWLSVQAKDPLWVAHMPCEVDER AKELNNFGDASVLIIDGQKIDLAGVNFKNSKTVEINGKTMVAVACCSNLE ISELNNFGDASVLIIDGKKIKLAGSGFTNKHTIEINGKTMVAVACCSNLE **	418 421 375

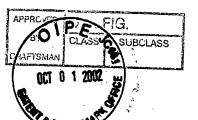


FIGURE 10B

25.00		
PHTBP1	HHKRRLGFTYKYKPENNRWLDSINSCVRALRSRCCALSKQDIELY	463
APL	YMKFGQLWQKEGKQQVKDNSLFLQGERTATDKMPAGGNYKYVGTWD	467
APL7	YMKFGQLWQQAEGGKPENNSLFLQGERTATDKMPKGGNYKYIGTWD	421
	. * * * *	
PHTBP1	SRLHRLHCSDYPVVDKNCGPTLDKSWSMYRTERNNYQEKATCHSFCI	510
APL	ALVSKGTNWIAEADNNRESGYRTEFDVNFSDKKVNGKLFDKGGVNPVFTV	517
APL7	AQVSKENNWVATADDDRKAGYRTEFDVDFGNKNLSGKLFDKNGVNPVFTV	471
	**	
PHTBP1	LKALNAGQGVFKQTHKLNLGLGFESNLIRLTIIGIILPNIPKAGYTSYRG	560
APL	DATIN-GNGFIGSAKTSDSGFALDAGSSQHGNAVFSDIKVNGGFYGPT	564
APL7	DAKID-GNGFTGKAKTSDEGFALDSGSSRYENVKFNDVAVSGGFYGPT	518
•	*.* *	
PHTBP1	RGRLDNPYIYRRDPRSIETVSLCNNTRATLLLLRVNKGIRLLLR 604	
APL	AGELGGQFHHKSDNGSVGAVFGAKRQIEK 593	
APL7	AAELGGQFHHKSENGSVGAVFGAKQQVKK 547	
	. * **	

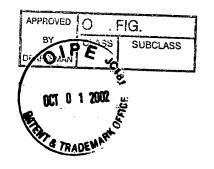
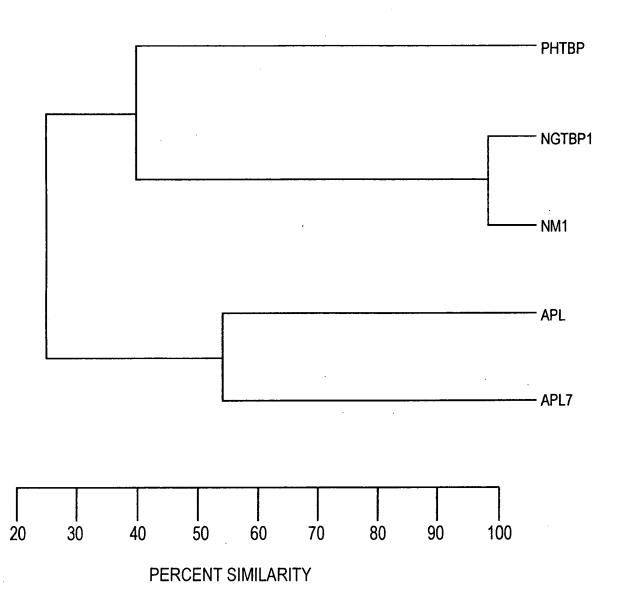


FIGURE 11



	1	TonB box	
	PHTBP1	DEVIVTE	22
	CIRP	ETMVVTA	12
	FBPAP	DTIVVTA	17
	FHUAP	DTITVTA	13
	PECAP	FTLSVDA	30
	2		
	PHTBP1	YAIRGVDKNRVSLLVDG	121
	CIRP	VSIRGLDSSYTLILVDG	105
	FEPAP	IDIRGMGPBNTLILIDG	102
	FHUAP	Liirgfaaegosonnyl-ng	141
n .	FECAP	FGIRGLNPRLTSRSTVLMDG	199

ñ			
	· _		
 ;	3	and an misson 1000 TOTPEVD	177
<u>بعقہ</u>	PHTBP1	IBLSKGASSABYGSGAHGGAIGFRTKD	159
wii:	CIRP	IBVVRGPMSSLYGSDALGGVVNIITKK IBVLRGPARARYGNGAAGGVVNIITKK	180
1	PEPAP	ABIMRGPVSVLYGKSSPGGLLNMVSKR	188
Ī	FHUAP	IDVVRGGGAVRYGPQSVGGVVNFVTRA	251
ī	FECAP	IDAAKGGGAAKIGAGAAMLAIKA	271
4 m fm fm m m m m m m m m m m m m m m m			
	4 PHTBP1	FKOTHKLNLGLGF	533
	CIRP	PETSESWELGLYY	461
	FEPAP	AETSINKEIGLEF	447
	FECAP	PSKGKQYEVGVKY	560
	FECAP	PEKARTWELGTRY	578
	LDCVL	· * ****** * ****	•

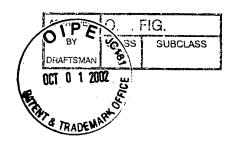
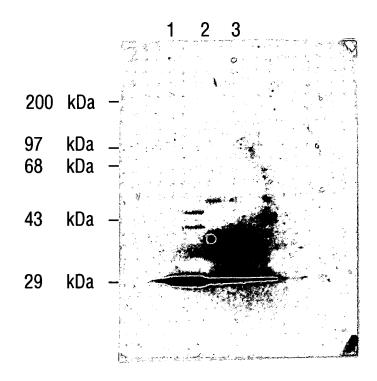
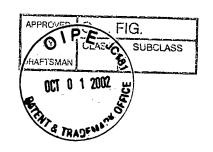


FIGURE 13





M 1 2 3 4 5 6 7 8

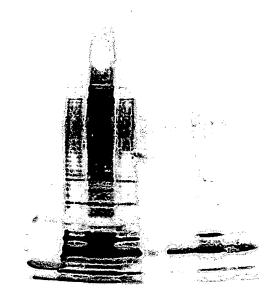
200 kDa –

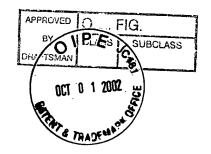
97 kDa –

68 kDa –

43 kDa –

29 kDa –





 $M \ 1 \ 2 \ 3 \ 4 \ 5 \ 6 \ 7 \ 8$

200 kDa –

97 kDa –

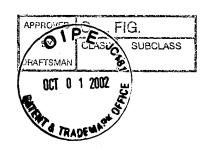
68 kDa -

43 kDa -

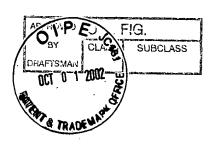
29 kDa -

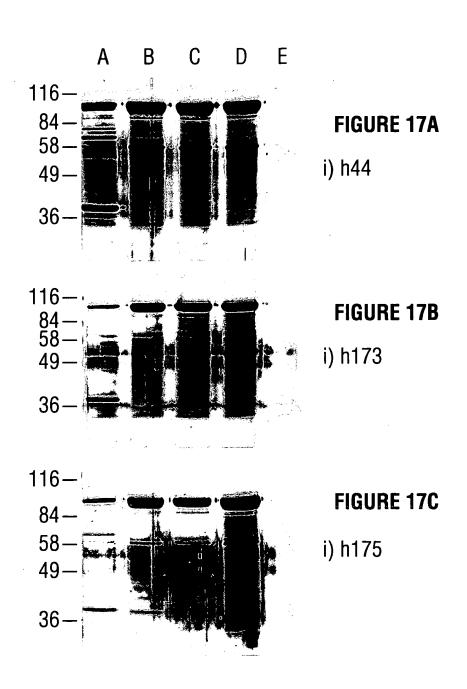


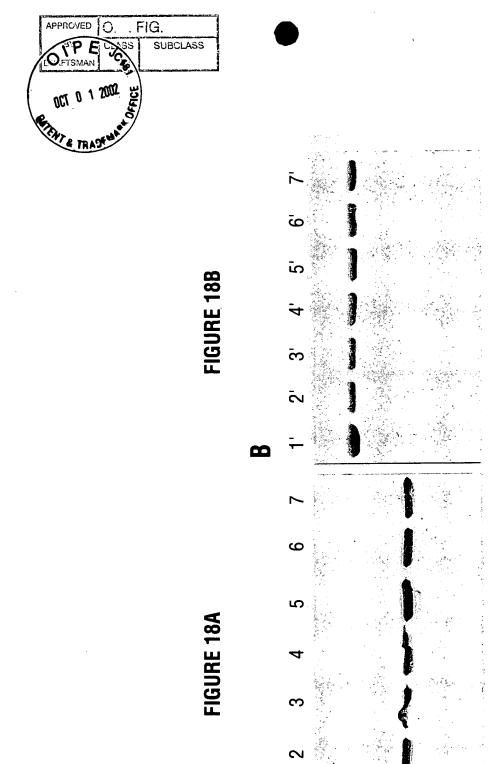




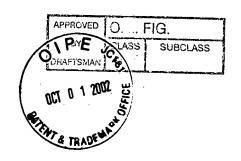
HRP bTf		HRP – cTf	HRP – eTf
h173 — 🦸	•		
h174 − •	•	•	
h175 − 👁	•	•	
h176 − •	•	•	
h44 − •	•	•	
h 50 —			







- 89



F	IGURE 19A	FIGURE 19B	FIGURE 19C
	HRP-bTf	Anti-Tbp1	Anti-Tbp2
h98	0.0		
h99			9
h100		0	•
h105	•		•
h106			
		8	,

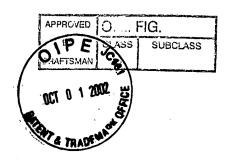
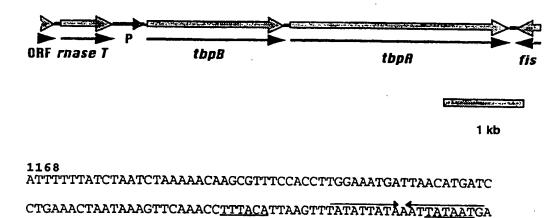


FIGURE 20A



-10

TTATTATTTATAAA<u>TTAAAGGAG</u>ACATT<u>ATG</u>TTTAAACTTAAAAGTAGTTTTGTA
SD Met₁₃₀₉

CTG.....tbpB....GAAAAA<u>TAA</u>TCATAATTCCCCTTTGCTGGTTGTAG

SC₃₀₆₃

ATAGCAAGCGGGCAATTTTTATAAAAAATTTGCAAAATTTAA<u>ATAAAGGAG</u>ACCCT

SD

ATCTA<u>ATG</u>ATAATGAAATATCATCATTTTCGC....tbpA......AGAAA

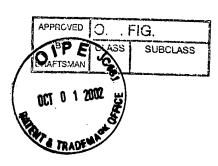
 ${\tt Met_{3151}} \\ {\tt TTTCAGTTTAGCATTTGAAATGAAGTTT\underline{TAG}}\,.$

SC₅₉₄₃

FIGURE 20B

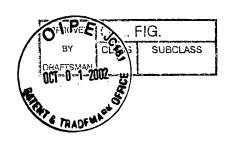
ATGATAATGAAATATCATCATTTTTCGCTATTCACCTGTTGCCTTAACAGTGTTATTTGCTC TTTCTCATTCATACGGTGCTGCGACTGAAAATAAAAAAATCGAAGAAAATAACGATCTAGC TGTTCTGGATGAAGTTATTGTGACAGAGAGCCATTATGCTCACGAACGTCAAAACGAAGTA ACTGGCTTGGGGAAAGTAGTGAAAAATTATCACGAAATGAGTAAAAATCAAATTCTTGGTA TTCGTGATTTAACTCGCTATGACCCTGGTATTTCGGTGGTGGAACAAGGTCGCGGTGCAAG TAGTGGCTATGCCATTCGAGGTGTAGATAAAAACCGTGTCAGCTTACTTGTTGATGGGCTA CCACAAGCGCACAGTTATCATACGCTAGGTTCAGATGCTAATGGTGGTGCAATTAATGAGA TTGAGTATGAAAACATTCGTTCAATTGAGTTAAGCAAAGGAGCAAGTTCTGCGGAATATGG CTCTGGTGCGCATGGTGCTATTGGTTTTCGTACTAAAGATĞCGCAGGATATTATTAAA GAGGGGCAGCATTGGGGCTTAGATAGTAAGACCTCTTATGCCAGCAAAAATAGCCATTTTT TACAGTCTATCGCAGCGGCTGGTGAGGCGGGTGGTTTTGAAGCACTTGTTATTGCAACTCĀ CGTATAACCGGCTTTGAAAATCGCTACGACTTTACCCAAATTCCGCACAGAATGCTCCTGG AGGATCTCCTTTTAATTGTGGAAGATACTTGCCCAACATTAGATTGTACTCCTCGTGCAAG GGTTAAGTTGAACCGCGATAATTTCCCAGTGAGAACATTTCCGGAATATACGCCTGAAGAG CGCAAACAGCTTGAGCAGATTCCTTATCGCACTGAGCAGCTCTCAGCCCAAGAATATACCG GTAAAGATCGCATTGCACCAAACCCTTTAGATTACAAGAGTAATTCTGTTTTTATGAAGTT TGGCTATCACTTCAACTCGTCTCATTATCTTGGCGCAATCTTAGAAGATACAAAAACACGC TACGATATCCGTGATATGCAAACGCCAGCTTACTATACAAAAGACGATATTAACTTATCAC TTAGGAACTATGTTTATGAAGGGGATAATATTTTAGATGGCTTAGTGTTCAAGCCAAGGAT CCCTTATGGGTTGCGCTATAGCCATGTGAAGTTTTTTGATGAACGTCACCACAAACGTCGŤ TTAGGATTCACCTATAAATATAAACCAGAGAATAATCGCTGGTTGGATAGCATTAAACTCA GTGCGGATAAACAAGATATTGAACTATATAGCCGGCTACATCGCTTGCATTGTAGCGATTA TCCTGTGGTAGATAAAATTGCCGCCCGACTTTGGATAAATCTTGGTCTATGTATCGAACT ATGCTGGTCAAGGCGTATTTAACCAAACCCACAAACTGAATTTAGGGTTGGGCTTTGATCG ATTTAATTCGCTTATGGATCATGGGGATATGACTGCCCAATATACCAAAGGCGGTTATACC AGCTACCGCGGTAGAGGGCGTTTAGATAATCCATATATTTATCGCCGCGATCCACGCAGTA TTGAAACGGTATCTTTGTGTAATAATACACGCGGCGACATCTTAAACTGTGAACCGCGTAA AATTAAAGGCGATAGCCATTTTGTTAGCTTCCGCGATCTAGTGATAAGCGAGTATGTGGAT TTGGGATTAGGGGTGCGTTTTGATCAACATCGATTTAAATCTGATGATCCGTGGACACTTĀ GCCGAACTTATCGAAATTGGTCTTGGAATGGTGGGATTACGCTTAAACCAACAGAGTTTGT ATCGCTTTCTTATCGCATTTCAAACGGTTTTAGAGTGCCTGCATTCTATGAACTTTATGGT AAACGTGATCATATTGGGCTTAAAGATAACGAATATGTGCAACGCGCGCAACGTAGCCACC AGTTAGAGCCAGAAAAATCGACTAATCATGAGATTGGAGTTAGCTTTAAAGGTCAATTTGG TTACCTTGATGTGAGCTATTTCCGTAATAACTATAAAAATATGATTGCGACAGCATGTAAA AGAATAATACAAAAATCACACTGTTTCTATAACTACCATAATATTCAAGATGTAGCACTAA ACGGGATAAATTTAGTCGCTAAATTTGACTTACACGGTATTTTATCTATGCTGCCAGATGG TTTTTATTCATCAGTTGCTTATAACCGTGTAAAAGTAAAAGAGCGGAAACTAACCGACTCA GATTCGGCTACGATCACCCAGAAGAAAAATGGGGAATTGGCATTACTACCACCTATTCTAA AGCCAAAAACGCCGATGAGGTGGCAGGCACACGTCATCACGGNATACATCGCGTTGATTTA GGTGGCAAACTGACCGGTTCTTGGTACACCCATGATATTACCGGTTACATCAATTATAAAA ACTACACCTTACGTGGAGGAATTTATAATGTGACTAATCGTAAATATTCCACTTGGGAATC AGTGCGCCAATCCGGTGTGAATGCAGTAAACCAAGACCGGGGTAGCAATTACACTCGATTT_ GGCGCTCCGGGGAGAAATTTCAGTTTAGCATTTGAAATGAAGTTTTAG

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211	$\underline{\mathbf{G}}$	E	Α	G	<u>G</u>	F	E	Α	L	V	<u>I</u>	A	<u>T</u>	H	<u>R</u>	H	G	K	E	Т	K	I	<u>H</u>	S	E	A	N	K	L	K
241	Η	N	I	R	R	I	T	G	F	E	N	R	Y	D	F	T	Q	I	P	Н	R	M	L	L	Е	D	L	L	L	I
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301	Y	T	P	E	E	R	K	Q	L	E	Q	I	P	Y	R	T	E	Q	L	S	Α	Q	Е	<u>Y</u>	<u>T</u>	<u>G</u>	K	D	<u>R</u>	I
331	Α	P	N	<u>P</u>	L	D	$\underline{\mathbf{Y}}$	K	<u>S</u>	N	<u>S</u>	V	F	M	K	F	Ġ	Y	H	F	N.	S	S	H	<u>Y</u>	L	G	A	Ĭ	L
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391	V	Y	Ε	G	D	N	I	L	D	G	L	V	F	K	P	R	I	P	Y	<u>G</u>	L	R	Y	S	Н	v	K	F	F	<u>D</u>
421	<u>E</u>	R	<u>H</u>	Н	K	R	<u>R</u>	Ĺ	G	F	Т	Y	K	Y	K	P	E	Ñ,	N	Ŕ	W	L	Ď	S	Ϊ	K	Ĺ	S	Ā	D
451	K	Q	D	Ī	E	L	Y	S	R	L	Η	R	L	H	<u>C</u>	<u>S</u>	D	Y	P	V	V	D	<u>K</u>	N	<u>C</u>	<u>R</u>	P	T	L	<u>D</u>
481	<u>K</u>	S	W	<u>S</u>	M	Y	R	T	E	R	N	N	$\underline{\mathbf{Y}}$	Q	<u>E</u>	K	<u>H</u>	R	V	I	H	L	Ë	F	D	K	Á	L	Ñ	A
511	G,	Q)	G	V,	F	N.	Q	T	H	K	L	N	L	G	L	G	F	<u>D</u>	R	F	N	<u>S</u>	L	M	D	H	G	D	M	T
541	Α	Q	Y	T	K	G	G	Y	T	S	Y	R	G	R	<u>G</u>	R	L	D	N	<u>P</u>	<u>Y</u>	I	Y	R	R	D	P	R	S	I
571	Ε	T	V	S	L	<u>C</u>	N	N	T	R	G	D	I	L	N	<u>C</u>	E	P	R	K	I	K	\mathbf{G}	D	S	H	F	V	S	F
601	R	D.	ĨL,	V.	Ĩ,	S	Ē	Ŷ	V	<u>D</u>	L	<u>G</u>	L	G	V	R	F	<u>D</u>	Q	Н	R	F	K	S	D	D	P	W	T	L
631	S	R	T	Y	R	N	W	S	W	<u>N</u>	G	<u>G</u>	Ī	T	L	<u>K</u>	<u>P</u>	T'	E	F	V	S	L	S	<u>Y</u>	<u>R</u>	Ι	<u>S</u>	N	<u>G</u>
661	<u>F</u> :	<u>R</u>	V	<u>P</u>	Α	<u>F</u>	Y	E	L	Y	G	K	R	D	H	I	G	L	K	D	N	E	Y	V	Q	R	A	Q	R	S
691	H									*****	****																			
721	<u>N</u> :	Ν	<u>Y</u>	K	N	M	Ī	Α	T	A	C	K	R	I	I	Q	K	S	H	C	F.	Y	N	Y	H	N	I	Q	D	V
751	Α	L	N	<u>G</u>	Ι	N	L	V	Α	K	F	D	L	Ĥ	<u>@</u>	<u>I</u>	L	8	M	ĨL,	<u>B</u>	D.	Œ	F	Y	S	S	٧	<u>A</u>	<u>Y</u>
781	N	R	V	K	Y	K	E	R	<u>K</u>	L	T	D	S	R	L	D	S	V	N	D	P	I	L	D	A	I	Q	<u>P</u>	Ą	<u>R</u>
811	<u>Y</u>	V	L	G	F	\mathbf{G}	<u>Y</u>	<u>D</u>	H	R	B	B	K	W	<u>G</u>	Ι	G	Ι	Т	Т	T	Y	<u>S</u>	K	Α	<u>K</u>	N	Α	D	<u>E</u>
841	KKKKKKKKKK	xxxxxxx	MACOON NO.	NOO OO OO	ONYMANA	WAY WAY	MANAGE P	SECONOMIA	MANAGES !			4.5		2000000	****	XXXXXX	2222		XXXXXX	228.24	222	****	223						G	
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																					CXXXX	**************************************	32.	33333		200	2	12000	didina.	Ditte.



ATGTTTAAACTTAAAAGTAGTTTTGTACTGCTTAATGCGGCGCTACTTGCTGCTTGTTCCT CAAATGGTGGAAGCTTTGATGTTCAATCTGCCAAAGTTGAATCTCAAACGCAAACTACCCC CAAAAAGCCAAGTTTACAAGATGATAATAGTAACGCAAGACGTACAGTAAGCGCTTCTGAA ACTGAAGCTTTATTGCAGCCGGGGTTTGGTTTTTCAGCCAAAATTCCGCGTCGTAATCTCC TTCCGCAGGGGAAGAAGATGTAGCCCCTATTGGTGATATAAAAGAGATTACTGGAGATCT GCCAAAAATTCCGTATGAAGAAGAGGTTAAAGCGTGCGGTAGTAGTGCTGATGGATTTAGC **ATGTTGTGCATTCTGGTCCAAAACCTGAAATAAAGCCTAAAGAAATTTTGAGAACAGGTGC** ACTTATAAAGGATATTGGGATTTTACTACCTATGCGGCTAAGGGGAGAGATAGTAATATTT TTCTAATTCCCGCAGGCATCAATAGTGGCGCCATACCGGAAAATAGTCACGATATTAATGT TGATGATTCTGAAAAACCAATGGGGCATACAGGAGAATTTACGGCTGATTTTGCTAATAAA ACTTTAACTGGAACATTGGTTCGTAATGGGTATGTTAGTCGTAGCAAAGAGCAAAAAATTA CAACAATTTACGATATTGATGCGAAAATTAAAGGTAATCGCTTTTCTGGTAAAGCAAACCC AAAAAAACCGATGATCCTTATTTTTGGGAAAAGCTCCACGACACTTGAAGGTGGATTTTTT GGTGGGGAGGCTCAAGAACTTGCCGGTAAATTCTTAGCTGATGATAAGTCGGTATTTGTTG TTTTTGCTGGCACACGAGATGCTAAAAAAGATGATAGTGAATCTGCCTTTGATGCTTTCCC **AATTAAACTTAAAGATTTAAATAAATCTGAGATGGATACTTTCGGGAATGCGACACATTTG** ATTATTAACAATAAGCAGATTCCACTTATTGCGGAAGCCACAAAAAGCTTTGCCGAGATGA AATTTGATGATTTGGTTACCCGTACTATTGATGGAAAAACGTATCGAGTTTCAGTCTGCTG TAATAATTTAGATTATGTCAAATTTGGGATTTATAGCGAGGGAAATAATAGTGATACTGCT CTCCAAGAATATTTAGTAGGAGAACGTACAGCTCTGGCAGATTTGCCAACAGGGACAGTAA **AATATCGAGGTACTTGGGACGGGGTAATGTACAGTAAATCTGGCTCGGCAGGGGTTGAATC** GCCAAGTAACAGCGAAAGTGGTACTCGTTCACTATTCGATGTAGATTTTGTCAATAAAAAA ATTAATGGCAAGCTGATTGCTAATGATGGTGTTGAAGAACGCCCAATGCTGACACTGGAAG GCAATCTGAAAGGGAATGGTTTTGGAGGCACAGCCAAAACGGGCAATTCTGGTTTTAATCT TGATCCCAAAAGTACGAATGGTGGCACGGTAGGGCATATAAATACTCAATTTGAAGGGGGC TTTTATGGCCCTAAGGCGACGGAATTAGGTGGTATTGTACAAAATACAGAAACGGATAAAG ATAGAGTCAGTATTACATTCGGCGGAAAACGTCAAATAGAAAAATAA

MFKLKSSFYLLNAAEEA<u>A</u>CSSNG<u>GSED</u>VQS 1 31 AKVESQTQTTP KKPSL QDD N S N A R R T V S A S ETEALLQPGFGFSAKIPRRNLLPQGKEDVA 61 P I G D I K E I T G D L P K I P Y E E E V K A C G S S A D G 91 F S H T H D R N H K L Y T R D F N F Y R S G Y V V H S G P K 121 P E I K P K E I L R T G A H <u>G Y V Y Y L G</u> I E P P K A I <u>P</u> T 151 QKLT<u>YKG</u>Y<u>W</u>DFTTYAAKGRDSNIFLIPAGI 181 211 N S G A I P E N S H D I N V D D S E K P M G H T G E F T A D E AN KTLTGT L VRNG YVSRSKEQKITT I YD I 241 DAKIKG<u>NRF</u>S<u>GK</u>ANPKKPMILIFGKSSTT<u>L</u> 271 EGGFFGGEAQELAGKFLADDKSVFVVFAGT 301 331 R D A K K D D S E S A F D A F P I K L K D L N K S E M D T F 361 GNATHLIINNKQIPLI AEATKS F AEMK F D D LVTRTIDGKTYRVSV<u>CCNNLDY</u>VKF<u>G</u>IYS E 391 GNNSDTALQEYLVGERTALADLPTGTVKYR 421 GTWDG VMYSKSGSAGVESPSNSESGTRSL F 451 D<u>V</u> D <u>F</u> V N <u>K</u> K I N <u>G</u> K <u>L</u> I A N DG V E E R P M L T L E G N 481 LKGNGEGGTAKTGNSGFNLDPKSTNGGTVG 511 н I N T Q F E G G F Y G P K A T E L G G I V Q N T E T D K D 541 RVSIT<u>FGGKRO</u>IEK 571



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	A. O.	Mai	A. S.
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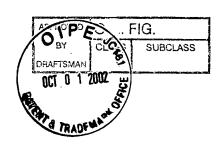


FIGURE 26A

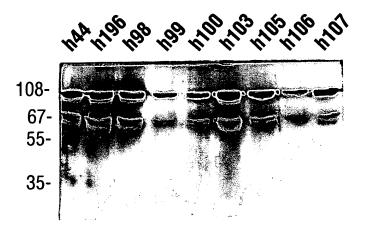
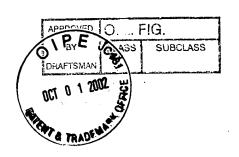
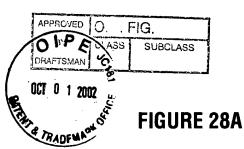


FIGURE 26B

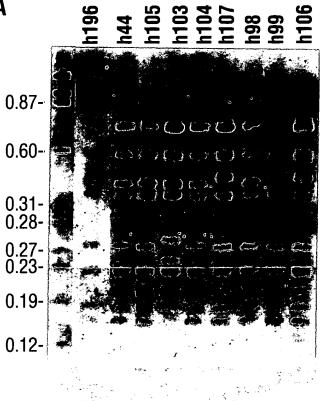


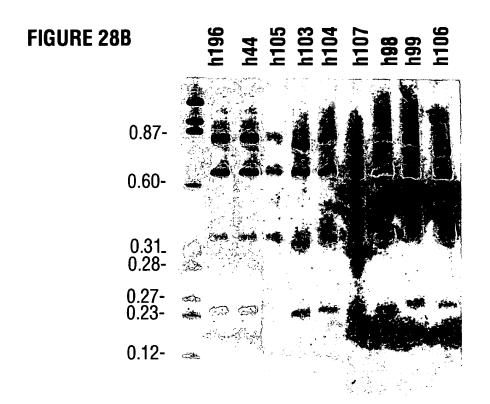


	HRP-bīf	Anti-TbpA	Anti-TbpB
h44 Fe +			Ö,
h44 Fe -	•	•	4
h196			
h98	•	((8
h99	•	•	
h100	0	· O	•
h103	•		· • ,
h105	•		
h106		Ó	
h107	0		



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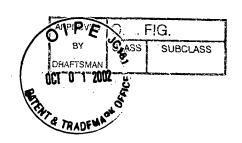


FIGURE 29A

h196 h99 h100 h104 h105 h105 h107 h107

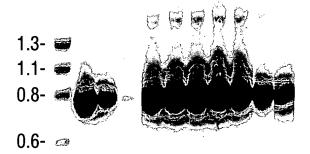


FIGURE 29B

h196 h99 h100 h103 h105 h105 h107 h174 h174

